PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/430,035*

AU 1812

DATE: 03/28/96
TIME: 11:48:15

INPUT SET: S9572.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5     (i)  APPLICANT: Eaton, Dan L.
 6                     de Sauvage, Frederic J.
 7
 8    (ii)  TITLE OF INVENTION: MPL LIGAND
 9
10   (iii)  NUMBER OF SEQUENCES: 21
11
12    (iv)  CORRESPONDENCE ADDRESS:
13           (A) ADDRESSEE: Genentech, Inc.
14           (B) STREET: 460 Point San Bruno Blvd
15           (C) CITY: South San Francisco
16           (D) STATE: California
17           (E) COUNTRY: USA
18           (F) ZIP: 94080
19
20     (v)  COMPUTER READABLE FORM:
21           (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
22           (B) COMPUTER: IBM PC compatible
23           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24           (D) SOFTWARE: WinPatin (Genentech)
25
26    (vi)  CURRENT APPLICATION DATA:
27           (A) APPLICATION NUMBER: 08/430035
28           (B) FILING DATE: 27-Apr-1995
29           (C) CLASSIFICATION:
30
31   (vii)  PRIOR APPLICATION DATA:
32           (A) APPLICATION NUMBER: 08/196689
33           (B) FILING DATE: 15-FEB-1994
34
35   (vii)  PRIOR APPLICATION DATA:
36           (A) APPLICATION NUMBER: 08/185607
37           (B) FILING DATE: 21-JAN-1994
38
39   (vii)  PRIOR APPLICATION DATA:
40           (A) APPLICATION NUMBER: 08/176553
41           (B) FILING DATE: 03-JAN-1994
42
43  (viii)  ATTORNEY/AGENT INFORMATION:
44           (A) NAME: Winter, Daryl B.
45           (B) REGISTRATION NUMBER: 32,637
46           (C) REFERENCE/DOCKET NUMBER: P0871P2D2
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/430,035*

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TIME: 11:48:18

INPUT SET: S9572.raw

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47
48      (ix) TELECOMMUNICATION INFORMATION:
49           (A) TELEPHONE: 415/225-1249
50           (B) TELEFAX: 415/952-9881
51           (C) TELEX: 910/371-7168
52
53   (2) INFORMATION FOR SEQ ID NO:1:
54
55       (i) SEQUENCE CHARACTERISTICS:
56           (A) LENGTH: 42 amino acids
57           (B) TYPE: Amino Acid
58           (D) TOPOLOGY: Linear
59
60     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62   Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
63   -16 -15                 -10                     -5
64
65   Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
66        1           5               10
67
68   Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
69    15              20               25  26
70
71   (2) INFORMATION FOR SEQ ID NO:2:
72
73       (i) SEQUENCE CHARACTERISTICS:
74           (A) LENGTH: 390 base pairs
75           (B) TYPE: Nucleic Acid
76           (C) STRANDEDNESS: Single
77           (D) TOPOLOGY: Linear
78
79     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
80
81
82   GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50
83
84   CACCTCTCCT CATCTAAGAA    TTG CTC CTC GTG GTC ATG CTT 91
85                           Leu Leu Leu Val Val Met Leu
86                           -16 -15                 -10
87
88   CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT CCT 130
89   Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro
90                   -5                      1
91
92   CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 169
93   Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg
94    5               10                      15
95
96   GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAACTCCCAA 210
97   Asp Ser His Val Leu His Ser Arg Leu
98           20               25  26
99
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INPUT SET: S9572.raw

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100    CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260
101
102    GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310
103
104    TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360
105
106    ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390
107
108    (2) INFORMATION FOR SEQ ID NO:3:
109
110        (i) SEQUENCE CHARACTERISTICS:
111            (A) LENGTH: 390 base pairs
112            (B) TYPE: Nucleic Acid
113            (C) STRANDEDNESS: Single
114            (D) TOPOLOGY: Linear
115
116       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
117
118
119    TCTAGACGAG AGCTTTTAAA TGCGGGCTGT ATTGTGAAGA ATAATTCTTG 50
120
121    TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100
122
123    GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150
124
125    TTACCAGTTA CGCGGATAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200
126
127    GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250
128
129    CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300
130
131    AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350
132
133    ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390
134
135    (2) INFORMATION FOR SEQ ID NO:4:
136
137        (i) SEQUENCE CHARACTERISTICS:
138            (A) LENGTH: 353 amino acids
139            (B) TYPE: Amino Acid
140            (D) TOPOLOGY: Linear
141
142       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
143
144    Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
145    -21 -20                   -15                 -10
146
147    Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
148        -5                   1                 5
149
150    Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
151     10                  15                  20
152
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```
153   Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
154    25              30                  35
155
156   Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
157    40              45                  50
158
159   Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
160    55              60                  65
161
162   Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
163    70              75                  80
164
165   Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
166    85              90                  95
167
168   Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
169   100             105                 110
170
171   Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
172   115             120                 125
173
174   Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
175   130             135                 140
176
177   Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
178   145             150                 155
179
180   Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
181   160             165                 170
182
183   Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
184   175             180                 185
185
186   Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
187   190             195                 200
188
189   Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
190   205             210                 215
191
192   Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
193   220             225                 230
194
195   Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
196   235             240                 245
197
198   Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
199   250             255                 260
200
201   Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
202   265             270                 275
203
204   Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
205   280             285                 290
```

INPUT SET: S9572.raw

```
206
207    Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
208    295             300             305
209
210    Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
211    310             315             320
212
213    Ser Gln Asn Leu Ser Gln Glu Gly
214    325             330     332
215
216    (2) INFORMATION FOR SEQ ID NO:5:
217
218       (i) SEQUENCE CHARACTERISTICS:
219           (A) LENGTH: 1798 base pairs
220           (B) TYPE: Nucleic Acid
221           (C) STRANDEDNESS: Single
222           (D) TOPOLOGY: Linear
223
224      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
225
226
227    GCGTCTTCCT ACCCATCTGC TCCCCAGAGG GCTGCCTGCT GTGCACTTGG 50
228
229    GTCCTGGAGC CCTTCTCCAC CCGGATAGAT TCCTCACCCT TGGCCCGCCT 100
230
231    TTGCCCCACC CTACTCTGCC CAGAAGTGCA AGAGCCTAAG CCGCCTCCAT 150
232
233    GGCCCCAGGA AGGATTCAGG GGAGAGGCCC CAAACAGGGA GCCACGCCAG 200
234
235    CCAGACACCC CGGCCAGA ATG GAG CTG ACT GAA TTG CTC CTC 242
236                      Met Glu Leu Thr Glu Leu Leu Leu
237                      -21 -20             -15
238
239    GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC 281
240    Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser
241             -10                 -5
242
243    AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT 320
244    Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser
245    1           5                   10
246
247    AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG 359
248    Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
249       15              20              25
250
251    AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC 398
252    Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
253             30              35
254
255    CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA 437
256    Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys
257    40              45              50
258
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